

Variability in the relative quantity of human DNA resulted from metagenomic analysis of gut microbiota

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Abstract

We conducted the comparative study of seven different methods of total DNA extraction from human feces. All these methods are recommended in protocols for metagenomic analysis of human gut microbiota. We studied the relative quantity of human DNA calculated from shotgun sequencing on a SOLiD 4 genetic analyzer of metagenomic samples. It was shown that either initial amount of feces or a method applied for total DNA extraction do not affect on final relative human DNA abundance, which is less than 1% in healthy people. Invariance of this parameter allows to consider increased abundance of human DNA in metagenomic samples as a potential marker of inflammatory bowel diseases. | Abstract available from the publisher.

Keywords

DNA extraction from feces, metagenomic analysis, shotgun sequencing